In the Claims:

The current status of all claims is listed below and supercedes all previous lists of claims.

Please cancel claims 51-68 and add new claims 69-100 as follows:

1-68.   (canceled).

69.   (new) A method for providing bacterial bioagent characterizing information comprising:

a) measuring or calculating a plurality of molecular masses corresponding to a plurality of amplification products, wherein the amplification products are 46 to 166 nucleobases in length, and wherein the amplification products are obtained by amplification of a segment of bacterial nucleic acid with a primer pair that hybridizes to nucleic acid of about one hundred or more bacterial bioagents at conserved regions that flank an intervening variable region;

b) interrogating a database with an identification query, wherein the identification query comprises a measured molecular mass of an amplification product 46 to 166 nucleobases in length of nucleic acid of a bacterial bioagent obtained upon amplification with the primer pair, and wherein the database comprises at least some members of the measured or calculated plurality of molecular masses of step a) wherein each member of the plurality of measured or calculated molecular masses is indexed to bacterial bioagent characterizing information;

c) delivering a response that comprises the bacterial bioagent characterization information generated by comparison of the measured molecular mass of step b) with the measured or calculated molecular masses of step a) contained in the database.

70.   (new) The method of claim 69 wherein the nucleic acid encodes ribosomal RNA or a protein involved in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, energy generation, uptake, or secretion.

71.   (new) The method of claim 69 wherein the bioagent characterizing information is a genus name.

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72.   (new) The method of claim 71 wherein the genus name is *Acinetobacter, Aeromonas, Bacillus, Bacteriodes, Bartonella, Bordetella, Borrelia, Brucella, Burkholderia, Campylobacter, Chlamydia, Chlamydophila, Clostridium, Coxiella, Enterococcus, Escherichia, Francisella, Fusobacterium, Haemophilus, Helicobacter, Klebsiella, Legionella, Leptospira, Listeria, Moraxella, Mycobacterium, Mycoplasma, Neisseria, Proteus, Pseudomonas, Rhodobacter, Rickettsia, Salmonella, Shigella, Staphylococcus, Streptobacillus, Streptomyces, Treponema, Ureaplasma, Vibrio,* or *Yersinia.*

73.   (new) The method of claim 69 wherein the bioagent characterizing information is a species name.

74.   (new) The method of claim 69 wherein the bioagent characterizing information is a strain name.

75.   (new) The method of claim 69 wherein the response is delivered via a network.

76.   (new) The method of claim 75 wherein the network is a local area network, a wide area network, or the internet.

77.   (new) The method of claim 69 wherein the measured molecular mass is measured by mass spectrometry.

78.   (new) The method of claim 77 wherein the mass spectrometry is electrospray Fourier transform ion cyclotron resonance mass spectrometry or electrospray time-of-flight mass spectrometry.

79.   (new) The method of claim 69 wherein the variable region has no greater than 5% sequence identity among the one hundred or more bacterial bioagents.

80.   (new) The method of claim 69 wherein the primer pair comprises at least one modified nucleobase.

81.   (new) The method of claim 80 wherein the modified nucleobase comprises 2,6-diaminopurine, propyne C, propyne T, phenoxazine, or G-clamp.

82.   (new) The method of claim 69 wherein the bacterial bioagent is a biological warfare agent.

83.   (new) The method of claim 82 wherein the biological warfare agent comprises *Bacillus anthracis, Yersinia pestis, Franciscella tularensis, Brucella suis, Brucella abortus, Brucella melitensis, Burkholderia mallei, Burkholderia pseudomalleii, Salmonella typhi, Rickettsia typhii, Rickettsia prowasekii, Coxiella burnetii, Rhodobacter capsulatus, Chlamydia pneumoniae, Escherichia coli, Shigella dysenteriae, Shigella flexneri, Bacillus cereus, Clostridium botulinum, Coxiella burnetti, Pseudomonas aeruginosa, Legionella pneumophila,* or *Vibrio cholerae.*

84.   (new) The method of claim 69 wherein the conserved regions have between 80-100% sequence identity among the one hundred or more bacterial bioagents.

85.   (new) A method for providing bacterial bioagent characterizing information comprising:

        a) measuring or calculating a plurality of base compositions corresponding to a plurality of amplification products 46 to 166 nucleobases in length obtained by amplification of a segment of bacterial nucleic acid with a primer pair that hybridizes to nucleic acid of about one hundred or more bacterial bioagents at conserved regions that flank an intervening variable region;

        b) interrogating a database with an identification query, wherein the identification query comprises a measured base composition of an amplification product 46 to 166 nucleobases in length of nucleic acid of a bacterial bioagent obtained upon amplification with the primer pair, and wherein the database comprises at least some members of the measured or calculated plurality of base compositions of step a) wherein each member of the plurality of measured or

calculated base compositions is indexed to bacterial bioagent characterizing information; and

c) delivering a response to said step of interrogating said database wherein said response comprises bacterial bioagent characterization information generated by comparison of said measured molecular mass of step b) with said measured or calculated base compositions of step a) contained in said database.

86.   (new) The method of claim 85 wherein the nucleic acid encodes ribosomal RNA or a protein involved in translation, replication, recombination, repair, transcription, nucleotide metabolism, amino acid metabolism, lipid metabolism, energy generation, uptake, or secretion.

87.   (new) The method of claim 85 wherein the bioagent characterizing information is a genus name.

88.   (new) The method of claim 87 wherein the genus name is *Acinetobacter, Aeromonas, Bacillus, Bacteriodes, Bartonella, Bordetella, Borrelia, Brucella, Burkholderia, Campylobacter, Chlamydia, Chlamydophila, Clostridium, Coxiella, Enterococcus, Escherichia, Francisella, Fusobacterium, Haemophilus, Helicobacter, Klebsiella, Legionella, Leptospira, Listeria, Moraxella, Mycobacterium, Mycoplasma, Neisseria, Proteus, Pseudomonas, Rhodobacter, Rickettsia, Salmonella, Shigella, Staphylococcus, Streptobacillus, Streptomyces, Treponema, Ureaplasma, Vibrio,* or *Yersinia.*

89.   (new) The method of claim 85 wherein the bioagent characterizing information is a species name.

90.   (new) The method of claim 85 wherein the bioagent characterizing information is a strain name.

91.   (new) The method of claim 85 wherein the response is delivered via a network.

92.   (new) The method of claim 91 wherein the network is a local area network, a wide area network, or the internet.

93.   (new) The method of claim 85 wherein the measured base composition is determined from a molecular mass measured by mass spectrometry.

94.   (new) The method of claim 93 wherein the mass spectrometry is electrospray Fourier transform ion cyclotron resonance mass spectrometer or an electrospray time-of-flight mass spectrometer.

95.   (new) The method of claim 85 wherein the variable region has no greater than 5% sequence identity among the one hundred or more bacterial bioagents.

96.   (new) The method of claim 85 wherein the primer pair comprises at least one modified nucleobase.

97.   (new) The method of claim 96 wherein the modified nucleobase comprises 2,6-diaminopurine, propyne C, propyne T, phenoxazine, or G-clamp.

98.   (new) The method of claim 85 wherein the bacterial bioagent is a biological warfare agent.

99.   (new) The method of claim 98 wherein the biological warfare agent comprises *Bacillus anthracis, Yersinia pestis, Franciscella tularensis, Brucella suis, Brucella abortus, Brucella melitensis, Burkholderia mallei, Burkholderia pseudomalleii, Salmonella typhi, Rickettsia typhii, Rickettsia prowasekii, Coxiella burnetii, Rhodobacter capsulatus, Chlamydia pneumoniae, Escherichia coli, Shigella dysenteriae, Shigella flexneri, Bacillus cereus, Clostridium botulinum, Coxiella burnetti, Pseudomonas aeruginosa, Legionella pneumophila, or Vibrio cholerae.*

100.   (new) The method of claim 85 wherein the conserved regions have between 80-100%

sequence identity among the one hundred or more bacterial bioagents.